vector systems that are claimed, and therefore Applicants believe there is no issue of enablement concerning these vectors, nor are Applicants arguing that vectors other than those that initiate transcription of dsRNA are enabled, as no other vectors are recited in the claims. For example, claims 1 and 3 recite that a cDNA library is constructed in a "vector in an orientation relative to a promoter(s) that initiates transcription of said cDNA or DNA to double stranded (ds) RNA." Therefore, to the extent that the rejection of the claims is based on any misunderstanding that Applicants recited other vectors in the claims, Applicants respectfully request reconsideration.

To the extent that the Examiner is referring to enablement of non-plasmid vectors for expression of dsRNA, Applicants respectfully request reconsideration. The claims are now limited to the nematode *C. elegans*. This organism is a well known, well studied research organism. A person of skill in the art in the field of *C. elegans* research knows of a variety of vectors (including plasmid and non-plasmid vectors) that can be used for expression of genes in *C. elegans*.

Moreover, the features of vectors that are required for use in the practice of the claimed invention are thoroughly illustrated in the application, i.e., the ability to initiate transcription of double stranded RNA for RNA interference. As demonstrated by the listing of different types of vectors useful in *C. elegans* above, one of ordinary skill in the art is familiar with other vectors that have or can be readily modified to have the properties required to practice the claimed invention, as well as the use of such vectors in the claimed methods.

The Examiner stated her agreement with Applicants' assertions that the generation of cDNA libraries and the choice of vectors for such is routine in the art.. Regarding the Examiner's uncertainty about introduction of an entire cDNA library into one or more cells (as in claim 1(b)), expressed in the paragraph spanning pages 3 and 4 of the Office Action, Applicants note the following. A library contains many individual vectors (e.g., plasmids) which contain different inserts. When a library is introduced into cells, each cell takes up one or more vector molecules, but unless the library is exceedingly simple, each cell does not take up a sufficient number of vectors to include the entire variety of library inserts. This is, of course, why libraries are introduced into multiple cells or organisms (as in the case of *C. elegans*), so that each insert contained in the library vector molecules is expressed in at least one cell or organism. The person of skill in the art then observes phenotypic changes and selects the cells or organisms that exhibit such a change. Once selected, the insert in the vector contained within the cell or

organism is isolated and sequenced to identify the gene responsible for the observed phenotypic change. Therefore, by exercise of routine experimentation, one of ordinary skill in the art can identify a gene that causes a phenotype.

Applicants respectfully request reconsideration of the claims in view of the amendments and reasoned statements made above. If the Examiner wishes to advance the prosecution, or if the amendment is unclear, then the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

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Amended Claims

1.(twice amended) A method of identifying DNA responsible for conferring a phenotype of a [nematode] *C. elegans* cell or organism, which method comprises

a) constructing a cDNA or genomic library of the DNA of said [nematode] *C. elegans* cell or organism in a vector in an orientation relative to a promoter(s) that initiates transcription of said cDNA or DNA to double stranded (ds) RNA upon binding of a transcription factor to said promoter(s),

b) introducing said library into one or more of said [nematode] *C. elegans* cells or organisms comprising said transcription factor, and

c) identifying a phenotype of said [nematode] *C. elegans* cell or organism comprising said library and identifying the DNA or cDNA fragment from said library responsible for conferring said phenotype.

3.(twice amended) A method of assigning function to a known DNA sequence which method comprises

a) identifying a homologue(s) of said known DNA sequence in a [nematode] *C. elegans* cell or organism,

b) isolating the relevant DNA homologue(s) or a fragment thereof from said [nematode] *C. elegans* cell or organism,

c) cloning said homologue or fragment thereof into a vector in an orientation relative to a promoter(s) that initiates transcription of dsRNA from said DNA homologue or fragment upon binding of a transcription factor to said promoter(s),

d) introducing said vector into said [nematode] *C. elegans* cell or organism from step a) comprising said transcription factor, and

e) identifying the phenotype of said [nematode] *C. elegans* cell or organism compared to wild type.

12.(twice amended) A method according to claim 11 wherein said selectable marker comprises a nucleotide sequence capable of inhibiting or preventing expression of a gene in said [nematode] *C. elegans* cell and which gene is responsible for conferring a phenotype.

14.(twice amended) A method according to claim 12 wherein said nucleotide sequence is a part of or identical to said gene sequence conferring said phenotype, and which nucleotide sequence is such as to permit integration of said vector by homologous recombination in the genome of said [nematode] *C. elegans* cell or organism and following said integration said nucleotide sequence is capable of inhibiting expression of said gene sequence conferring said phenotype.

20.(twice amended) A method according to any of claims 1 or 3 wherein said [nematode] *C. elegans* cell or organism is contacted with a specified compound for screening for a desired phenotype.

38.(twice amended) A method of validating clones identified in yeast two hybrid vector experiments which method comprises

a) providing a construct including the DNA encoding the protein identified in the two hybrid vector experiment, which construct is such that said DNA is orientated relative to a promoter(s) that initiates transcription of said DNA to double stranded RNA upon binding of a transcription factor to said promoter(s),

b) transforming a [nematode] *C. elegans* cell or organism comprising said transcription factor with said construct, and

c) identifying a phenotypic change in said [nematode] *C. elegans* cell or organism when compared to a wild type.

92.(amended) A method according to claim 20 wherein said desired phenotype is resistance or sensitivity to said compound when compared to the wild type [nematode] *C. elegans* cell or organism.